







RAW SEQUENCE LISTING

DATE: 08/01/2000 TIME: 15:07:56

PATENT APPLICATION: US/09/427,873

Input Set : A:\09427873.txt Output Set: N:\CRF3\08012000\I427873.raw

## ENTERED

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SEQUENCE LISTING
       4 (1) GENERAL INFORMATION:
              (i) APPLICANT: Boyd, Michael R.
                               Gustafson, Kirk R.
                               Shoemaker, Robert H.
                               McMahon, James B.
             (ii) TITLE OF INVENTION: ANTIVIRAL PROTEINS AND PEPTIDES, DNA
                                         CODING SEQUENCES THEREFOR, AND USES THEREOF
            (iii) NUMBER OF SEQUENCES: 4
             (iv) CORRESPONDENCE ADDRESS:
                    (A) ADDRESSEE: Leydig, Voit & Mayer, Ltd.
                    (B) STREET: Two Prudential Plaza, Suite 4900
                    (C) CITY: Chicago
     19
     20
                    (D) STATE: IL
     21
                    (E) COUNTRY: U.S.A.
     22
                    (F) ZIP: 60601-6780
              (V) COMPUTER READABLE FORM:
                    (A) MEDIUM TYPE: Floppy disk
                   (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
     26
     27
     28
                    (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
             (vi) CURRENT APPLICATION DATA:
C~-> 31
                    (A) APPLICATION NUMBER: US/09/427,873
C--> 32
                    (B) FILING DATE: 27-Oct-1999
     33
                    (C) CLASSIFICATION:
     35
            (vii) PRIOR APPLICATION DATA:
     36
                   (A) APPLICATION NUMBER: 08/429,965
     37
                   (B) FILING DATE:
     39
           (viii) ATTORNEY/AGENT INFORMATION:
     40
                   (A) NAME: Larcher, Carol
     41
                   (B) REGISTRATION NUMBER: 35243
            (C) REFERENCE/DOCKET NUMBER: 61037
(ix) TELECOMMUNICATION INFORMATION:
        (A) TELEPHONE: (312)616-5600
(B) TELEFAX: (312)616-5700
(2) INFORMATION FOR SEQ ID NO: 1:
     45
     46
     49
     51
              (i) SEQUENCE CHARACTERISTICS:
     52
                   (A) LENGTH: 327 base pairs
     53
                   (B) TYPE: nucleic acid
                   (C) STRANDEDNESS: double
     55
                   (D) TOPOLOGY: linear
     57
            (ii) MOLECULE TYPE: DNA (genomic)
     60
            (ix) FEATURE:
                   (A) NAME/KEY: CDS
                   (B) LOCATION: 10..312
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
    67 CGATCGAAG CTT GGT AAA TTC TCC CAG ACC TGC TAC AAC TCC GCT ATC
```





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68																	
69				1				5					LO				
	CAG																96
	Gln		Ser	Val	Leu	Thr		Thr	Cys	Glu	Arg		Asn	Gly	Gly	Tyr	
73		15					20					25					
	AAC																144
	Asn	Thr	Ser	Ser	Ile	Asp	Leu	Asn	Ser	Val	Ile	Glu	Asn	Val	Asp	Gly	
77	30					35					40					45	
	TCC																192
80	Ser	Leu	Lys	Trp	Gln	Pro	Ser	Asn	Phe	Ile	Glu	Thr	Cys	Arg	Asn	Thr	
81					50					55					60		
83	CAG	CTG	GCT	GGT	TCC	TCC	GAA	CTG	GCT	GCT	GAA	TGC	AAA	ACC	CGT	GCT	240
84	Gln	Leu	Ala	Gly	Ser	Ser	Glu	Leu	Ala	Ala	Glu	Cys	Lys	Thr	Arg	Ala	
85				65					70			_	•	75	-		
87	CAG	CAG	TTC	GTT	TCC	ACC	AAA	ATC	AAC	CTG	GAC	GAC	CAC	ATC	GCT	AAC	288
	Gln																
89			80					85					90				
	ATC	GAC		ACC	CTG	AAA	TAC		таас	TCGA	GA T	CGTA					327
	Ile												•				34,
93		95	<b>-</b> 2			-,-	100	014									
	(2)		רבאקו	מסדי	₽O₽	SEO		ιO · 3									
98	(2)							STIC									
99		(1)						ino									
100	,			B) T					acru	.5							
			,	•													
		, 2 2	01 (D) TOPOLOGY: linear														
	03 (ii) MOLECULE TYPE: protein 05 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:																
		•	•				-			TD 11							
105	,	(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ				.,	<b>a</b> 1		_	
107	Leu	(xi	) SE	QUEN	CE D Ser	ESCR Gln	IPTI	ON:	SEQ	Asn	Ser		Ile	Gln	_	Ser	
107 108	Leu 1	(xi Gly	) SE	QUEN Phe	CE D Ser 5	ESCR Gln	IPTI Thr	ON: Cys	SEQ Tyr	Asn 10	Ser	Ala			15	;	
107 108 110	Leu 1 Val	(xi Gly	) SE	QUEN Phe Ser	CE D Ser 5 Thr	ESCR Gln	IPTI Thr	ON: Cys	SEQ Tyr Thr	Asn 10 Asn	Ser	Ala		Asn	15 Thr	;	
107 108 110	Leu 1 Val	(xi Gly Leu	) SE Lys Thr	QUEN Phe Ser 20	CE D Ser 5 Thr	ESCR Gln Cys	IPTI Thr Glu	ON: Cys Arg	SEQ Tyr Thr 25	Asn 10 Asn	Ser Gly	Ala Gly	Tyr	Asn 30	15 Thr	Ser	
107 108 110 111 113	Leu Leu Val Ser	(xi Gly Leu	Lys Thr	QUEN Phe Ser 20 Leu	CE D Ser 5 Thr	ESCR Gln Cys	IPTI Thr Glu	ON: Cys Arg	SEQ Tyr Thr 25	Asn 10 Asn	Ser Gly	Ala Gly	Tyr Gly	Asn 30 Ser	15 Thr	Ser	
107 108 110 111 113 114	Leu 1 Val Ser	(xi Gly Leu Ile	Lys Thr Asp	QUEN Phe Ser 20 Leu	CE D Ser 5 Thr	ESCR Gln Cys	Thr Glu Val	ON: Cys Arg Ile 40	SEQ Tyr Thr 25 Glu	Asn 10 Asn Asn	Ser Gly Val	Ala Gly Asp	Tyr Gly 45	Asn 30 Ser	15 Thr	Ser Lys	
107 108 110 111 113 114 116	Leu 1 Val Ser	(xi Gly Leu Ile	Lys Thr Asp 35	QUEN Phe Ser 20 Leu	CE D Ser 5 Thr	ESCR Gln Cys	Thr Glu Val	ON: Cys Arg Ile 40	SEQ Tyr Thr 25 Glu	Asn 10 Asn Asn	Ser Gly Val	Ala Gly Asp Asn	Tyr Gly 45 Thr	Asn 30 Ser	15 Thr	Ser Lys	
107 108 110 111 113 114 116 117	Leu 1 Val Ser	(xi Gly Leu Ile Gln 50	Lys Thr Asp	QUEN Phe Ser 20 Leu	CE D Ser 5 Thr Asn	Cys Ser Phe	TPTI Thr Glu Val	ON: Cys Arg Ile 40	SEQ Tyr Thr 25 Glu Thr	Asn 10 Asn Asn Cys	Ser Gly Val Arg	Ala Gly Asp Asn 60	Tyr Gly 45 Thr	Asn 30 Ser Gln	15 Thr Leu	Ser Lys Ala	
107 108 110 111 113 114 116 117	Leu Val Ser Trp	(xi Gly Leu Ile Gln 50	Lys Thr Asp	QUEN Phe Ser 20 Leu	CE D Ser 5 Thr Asn	ESCR Gln Cys Ser Phe	Thr Glu Val Ile 55 Ala	ON: Cys Arg Ile 40	SEQ Tyr Thr 25 Glu Thr	Asn 10 Asn Asn Cys	Ser Gly Val Arg	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	15 Thr Leu	Ser Lys Ala	
107 108 110 111 113 114 116 117 119	Leu 1 Val Ser Trp Gly	(xi Gly Leu Ile Gln 50 Ser	Lys Thr Asp 35 Pro	QUEN Phe Ser 20 Leu Ser	CE E Ser 5 Thr Asn Asn	Cys Ser Phe Ala	Thr Glu Val Ile 55 Ala	ON: Cys Arg Ile 40 Glu	SEQ Tyr Thr 25 Glu Thr	Asn 10 Asn Asn Cys	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 119 120 122	Leu 1 Val Ser Trp Gly 65	(xi Gly Leu Ile Gln 50 Ser	Lys Thr Asp 35 Pro	QUEN Phe Ser 20 Leu Ser	CE E Ser 5 Thr Asn Asn Leu Ile	ESCR Gln Cys Ser Phe Ala 70	Thr Glu Val Ile 55 Ala	ON: Cys Arg Ile 40 Glu	SEQ Tyr Thr 25 Glu Thr	Asn 10 Asn Asn Cys	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 119 120 122 123	Leu Val Ser Trp Gly 65	(xi Gly Leu Ile Gln 50 Ser	Lys Thr Asp 35 Pro Ser	QUEN Phe Ser 20 Leu Ser Glu	CE D Ser 5 Thr Asn Asn Leu Ile 85	Cys Ser Phe Ala 70 Asn	Thr Glu Val Ile 55 Ala	ON: Cys Arg Ile 40 Glu	SEQ Tyr Thr 25 Glu Thr	Asn 10 Asn Asn Cys	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 119 120 122 123	Leu 1 Val Ser Trp Gly 65	(xi Gly Leu Ile Gln 50 Ser	Lys Thr Asp 35 Pro Ser	QUEN Phe Ser 20 Leu Ser Glu	CE D Ser 5 Thr Asn Asn Leu Ile 85	Cys Ser Phe Ala 70 Asn	Thr Glu Val Ile 55 Ala	ON: Cys Arg Ile 40 Glu	SEQ Tyr Thr 25 Glu Thr	Asn 10 Asn Asn Cys Lys	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 119 120 122 123	Leu Val Ser Trp Gly 65 Val	(xi Gly Leu Ile Gln 50 Ser	Lys Thr Asp 35 Pro Ser	QUEN Phe Ser 20 Leu Ser Glu	CE D Ser 5 Thr Asn Asn Leu Ile 85	Cys Ser Phe Ala 70 Asn	Thr Glu Val Ile 55 Ala	ON: Cys Arg Ile 40 Glu	SEQ Tyr Thr 25 Glu Thr	Asn 10 Asn Asn Cys Lys	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 119 120 122 123 125	Leu Val Ser Trp Gly 65 Val	(xi Gly Leu Ile Gln 50 Ser Ser	Thr Asp 35 Pro Ser Thr	QUEN Phe Ser 20 Leu Ser Glu Lys Tyr 100	CE D Ser 5 Thr Asn Asn Leu Ile 85 Glu	ESCR Gln Cys Ser Phe Ala 70 Asn	Thr Glu Val Ile 55 Ala	ON: Cys Arg Ile 40 Glu Glu Asp	SEQ Tyr Thr 25 Glu Thr Cys Asp	Asn 10 Asn Asn Cys Lys	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 119 120 122 123 125 128 130	Leu 1 Val Ser Trp Gly 65 Val Thr	(xi Gly Leu Ile Gln 50 Ser Ser Leu INF	Thr Asp 35 Pro Ser Thr Lys	QUEN Phe Ser 20 Leu Ser Glu Lys Tyr 100 TION	CE D Ser 5 Thr Asn Asn Leu Ile 85 Glu	ESCR Gln Cys Ser Phe Ala 70 Asn	Thr Glu Val Ile 55 Ala Leu	ON: Cys Arg Ile 40 Glu Glu Asp	SEQ Tyr Thr 25 Glu Thr Cys Asp	Asn 10 Asn Asn Cys Lys	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 120 122 123 125 126	Leu 1 Val Ser Trp Gly 65 Val Thr	(xi Gly Leu Ile Gln 50 Ser Ser Leu INF	Lys Asp 35 Pro Ser Thr Lys ORMA	QUEN  Ser  20  Leu  Ser  Glu  Lys  Tyr  100  TION  QUEN	CE D Ser 5 Thr Asn Asn Leu 11e 85 Glu FOR CE C	ESCR Gln Cys Ser Phe Ala 70 Asn SEQ HARA	TPTI Thr Glu Val Ile 55 Ala Leu ID CTER	ON: Cys Arg Ile 40 Glu Glu Asp	SEQ Tyr Thr 25 Glu Thr Cys Asp	Asn Asn Cys Lys His	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 119 120 122 123 125 128 130	Leu 1 Val Ser Trp Gly 65 Val Thr	(xi Gly Leu Ile Gln 50 Ser Ser Leu INF	Lys Asp 35 Pro Ser Thr Lys ORMA ) SE	QUEN Ser 20 Leu Ser Glu Lys Tyr 100 TION QUEN A) L	CE D Ser 5 Thr Asn Asn Leu 11e 85 Glu FOR CE CE	ESCR Gln Cys Ser Phe Ala 70 Asn SEQ HARA H: 3	TPTI Thr Glu Val Ile 55 Ala Leu ID CTER 27 b	ON: Cys Arg Ile 40 Glu Glu Asp NO: ISTI	SEQ Tyr Thr 25 Glu Thr Cys Asp 3: CS: pair	Asn Asn Cys Lys His	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 1111 113 114 116 117 120 122 123 125 126 130 131	Leu Val Ser Trp Gly 65 Val Thr	(xi Gly Leu Ile Gln 50 Ser Ser Leu INF	Lys Asp 35 Pro Ser Thr Lys ORMA ) SE	QUEN Ser 20 Leu Ser Glu Lys Tyr 100 TION QUEN A) L	CE D Ser 5 Thr Asn Asn Leu Ile 85 Glu FOR CE C ENGT YPE:	ESCR Gln Cys Ser Phe Ala 70 Asn SEQ HARA H: 3	TPTI Thr  Glu  Val  Ile 55 Ala  Leu  ID CTER 27 b leic	ON: Cys Arg Ile 40 Glu Glu Asp NO: ISTI ase	SEQ Tyr Thr 25 Glu Thr Cys Asp 3: CS: pair d	Asn Asn Cys Lys His	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 111 113 114 116 117 120 122 123 125 126 130 131 132	Leu 1 Val Ser Trp 65 Val Thr	(xi Gly Leu Ile Gln 50 Ser Ser Leu INF	) SE Lys Thr Asp 35 Pro Ser Thr Lys ORMA ( ( ( (	QUEN Ser 20 Leu Ser Glu Lys Tyr 100 TION QUEN A) L	CE CE Ser 55 Thr 55 Thr Asn Asn Leu 11ee 85 Glu FOR CE CE CENGT TRAN	ESCR Gln Cys Ser Phe Ala 70 Asn SEQ HARA H: 3 nuc	IPTI Thr Glu Val Ile 55 Ala Leu ID CTER 27 b leic ESS:	ON: Cys Arg Ile 40 Glu Glu Asp NO: ISTI ase aci dou	SEQ Tyr Thr 25 Glu Thr Cys Asp 3: CS: pair d	Asn Asn Cys Lys His	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 1113 114 116 117 120 122 123 125 126 128 130 131 132 133	Leu 1 Val Ser Trp 65 Val Thr	(xi Gly Leu Ilee Glnn 50 Ser Ser Leu INF (i	) SE Lys Thr Asp 35 Pro Ser Thr Lys ORMAA ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( ( (	CQUENT Phe Ser 200 Leu Ser Glu Lys Tyrr 1000 TIONN A) L B) T C) S C) S C) S C) S C) T C) S C) S C	CE C Ser 5 5 Thr Asn Asn Leu 85 Glu FOR CE CENGT YPE: TRAN OPOL	ESCR Gln Cys Ser Phe Ala 70 Asn SEQ HARA H: 3 nuc DEDN	IPTI Thr Glu Val Ile 55 Ala Leu ID CTER 27 b leic ESS:	ON: Cys Arg Ile 40 Glu Asp NO: ISTI ase dou ear	SEQ Tyr Thr 25 Glu Thr Cys Asp 3: CS: pair d	Asn 10 Asn Asn Cys Lys 90	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	
107 108 110 1113 114 116 117 120 122 123 125 126 128 130 131 132 133 133	Leu 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Leu Ile Gln 50 Ser Leu INF (ii	) SE Lys Thr Asp 35 Pro Ser Thr Lys ORMA ( ( ( ( ) MO	CQUENT Phe Ser 200 Leu Ser Glu Lys Tyrr 1000 TIONN A) L B) T C) S C) S C) S C) S C) T C) S C) S C	CE C Ser	ESCR Gln Cys Ser Phe Ala 70 Asn SEQ HARA H: 3 nuc DEDN	IPTI Thr Glu Val Ile 55 Ala Leu ID CTER 27 b leic ESS:	ON: Cys Arg Ile 40 Glu Glu Asp NO: ISTI ase aci dou	SEQ Tyr Thr 25 Glu Thr Cys Asp 3: CS: pair d	Asn 10 Asn Asn Cys Lys 90	Ser Gly Val Arg Thr 75	Ala Gly Asp Asn 60 Arg	Tyr Gly 45 Thr	Asn 30 Ser Gln	Thr Leu Leu Gln	Ser Lys Ala Phe 80	





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Input Set : A:\09427873.txt
Output Set: N:\CRF3\08012000\I427873.raw

140	140 (A) NAME/KEY: CDS																
141		(B) LOCATION: 1327															
144		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:															
146	GAC	TAC	AAG	GAC	GAC	GAT	GAC	AAG	CTT	GGT	AAA	TTC	TCC	CAG	ACC	TGC	48
147	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Leu	Gly	Lys	Phe	Ser	G1n	Thr	Cys	
148	ī	•	•	-	5	_				10					15		
150	TAC	AAC	TCC	GCT	ATC	CAG	GGT	TCC	GTT	CTG	ACC	TCC	ACC	TGC	GAA	CGT	96
151	Tyr	Asn	Ser	Ala	Ile	Gln	Gly	Ser	Val	Leu	Thr	Ser	Thr	Cys	Glu	Arg	
152			/	20					25					30			
					TAC												144
155	Thr	Asn	Gly	Gly	Tyr	Asn	Thr	Ser	Ser	Ile	Asp	Leu	Asn	Ser	Val	Ile	
156			35					40					45				
					GGT												192
159	Glu	Asn	Val	Asp	Gly	Ser	Leu	Lys	Trp	Gln	Pro	Ser	Asn	Phe	Ile	Glu	
160		50					55					60					
					ACC												240
163	Thr	Cys	Arg	Asn	Thr		Leu	Ala	Gly	Ser		Glu	Leu	Ala	Ala		
164	65					70					75					80	
					GCT												288
	Cys	Lys	Thr	Arg	Ala	Gln	Gln	Phe	Val		Thr	Lys	Ile	Asn		Asp	
168					85					90					95		
					AAC												327
	Asp	His	Ile		Asn	Ile	Asp	Gly		Leu	Lys	Tyr	Glu				
172				100					105								
	(2)				FOR	-											
177		(i		-	CE CI												
178			•	,	ENGT				acı	ıs							
179			,	,	PE:												
180					OPOLO												
182		(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:															
184													cor	Cln	mhr	Cuc	
187		TYL	гуу	ASP	Asp 5	ASP	ASP	пуѕ	Leu	10	пÃ2	Pile	ser	GIII	15	Cys	
	1	7.00	Com	11-	Ile	Cln	C1.,	Cor	W = 1		mhr	Cor	mhr	Cuc		λνα	
190	LĀT	ASII	261	20	TTE	GTII	GLY	261	25	Leu	1111	361	1111	30	GIU	arg	
	Thr	λen	Clv		Tyr	Aen	Whr	Sor		Tla	Δen	T.e.u	Δen		Val	Tle	
193	1111	ASII	35	GLY	1 1 1	ASII	1111	40	261	110	пор	БСи	45	JCI	vul	110	
	Clu	λen		\ en	Gly	Sar	I.ou		Ψrn	Gln	Pro	Ser		Phe	Tle	Glu	
196	Giu	50	vai	nap	Gry	36.1	55	Lys	1+12	OIII	110	60	11511	1 110	110	O-Lu	
	Thr		Ara	Asn	Thr	Gln		Ala	G1 v	Ser	Ser		Leu	Ala	Ala	Glu	
199	65	0,0	9			70			U-1		75					80	
		Lvs	Thr	Arq	Ala		Gln	Phe	Val	Ser	Thr	Lvs	Ile	Asn	Leu	Asp	
202	-,-	-1-			85					90			-		95	-	
	qzA	His	Ile	Ala	Asn	Ile	Asp	Gly	Thr	Leu	Lys	Tyr	Glu				
205	·- L			100				4	105		•	•					





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Input Set : A:\09427873.txt
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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]